## WHAT IS CLAIMED IS:

1. A method for the relative quantification of the methylation of cytosine bases in DNA samples, characterized in that the following method steps are conducted:

a) a genomic DNA sample is chemically reacted with a reagent, wherein 5-methylcytosine and cytosine react differently and these thus show a different base pairing behavior in the DNA duplex after the reaction;

b) the DNA sample is amplified, whereby a fluorescently labeled dCTP or dGTP derivative is added;

c) the amplified products are separated spatially from each other; and

d) the fluorescence of the separated amplified products is quantitatively measured.

2. The method according to claim 1, further characterized in that the amplified DNA sample is hybridized to one or more immobilized Oligomers, whereby the immobilized oligomers hybridize at least to one of the primers or their complementary sequences used in the amplification step in order to achieve the spatial separation.

3. The method according to claim 1, further characterized in that the amplified products from step (b) are separated by electrophoresis or chromatography.

4. The method according to claim 3, further characterized in that the separation is achieved by capillary gel electrophoresis.

5. The method according to claim 3, further characterized in that the separation is achieved by high pressure liquid chromatography (HPLC).

6. The method according to claim 1, further characterized in that a bisulfate solution is used in step (a) as the reagent.

7. The method according to claim 1, further characterized in that PCR is used in step (b) for the amplification.

8. The method according to claim 1, further characterized in that in step (b) the fluorescently labeled dCTP or dGTP derivative is Cy3-dCTP, Cy5-dCTP, Cy3-dGTP or Cy5-dGTP.

9. The method according to claim 1, further characterized in that the fluorescent dyes Cy3 and/or Cy5 are used as the label.

10. The method according to claim 1, further characterized in that an array of oligomers complementary or identical to the primers of step (b) is used for the hybridizing of the amplified products in step (c).

11. The method according to claim 1, further characterized in that the amplification of several DNA segments in step (b) is conducted simultaneously.

12. The method according to claim 1, wherein the values measured in step (d) are equilibrated with the fluorescence of other, analogously treated DNA samples and in this way information is obtained on the relative degree of methylation of different tissues or different cell samples.

13. The method according to one of the preceding claims, further characterized in that fluorescently labeled primers are used in the amplification step, wherein their fluorescent labeling is different from that of the dCTP or dGTP derivatives.